

Fig. 1

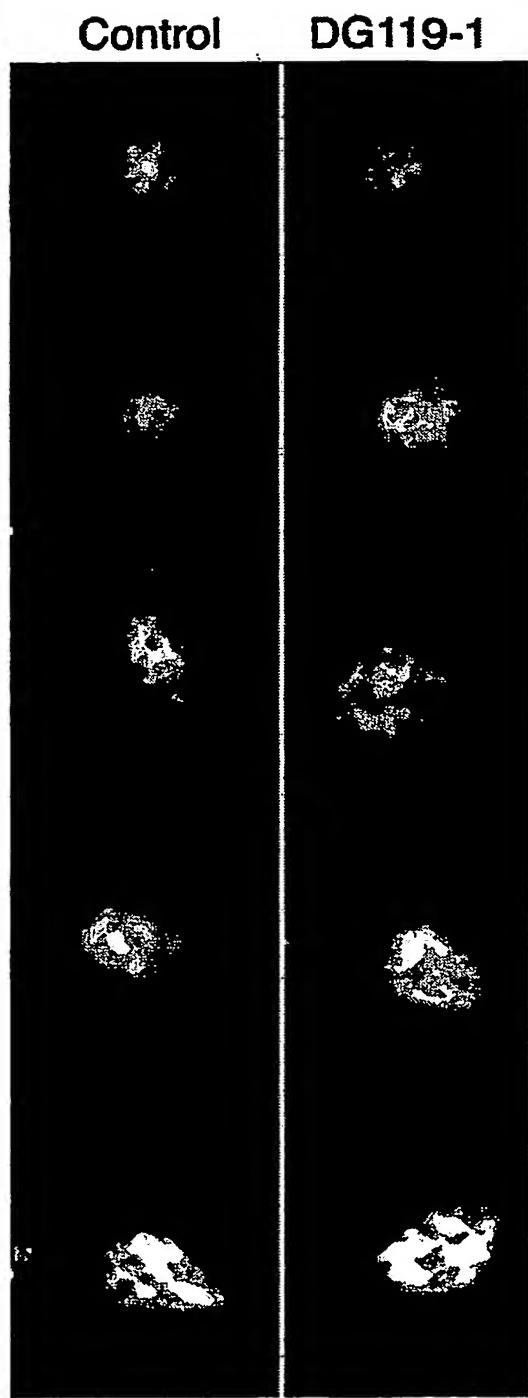


Fig. 2

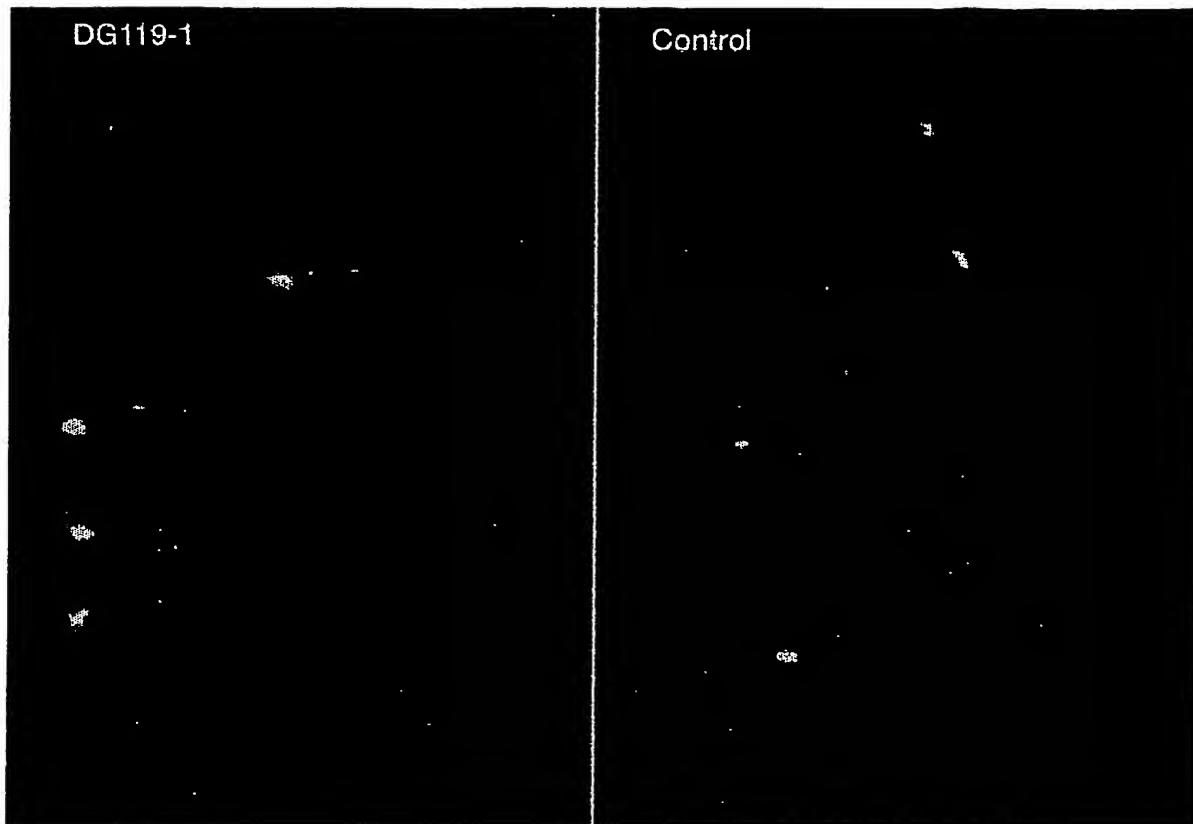


Fig. 3

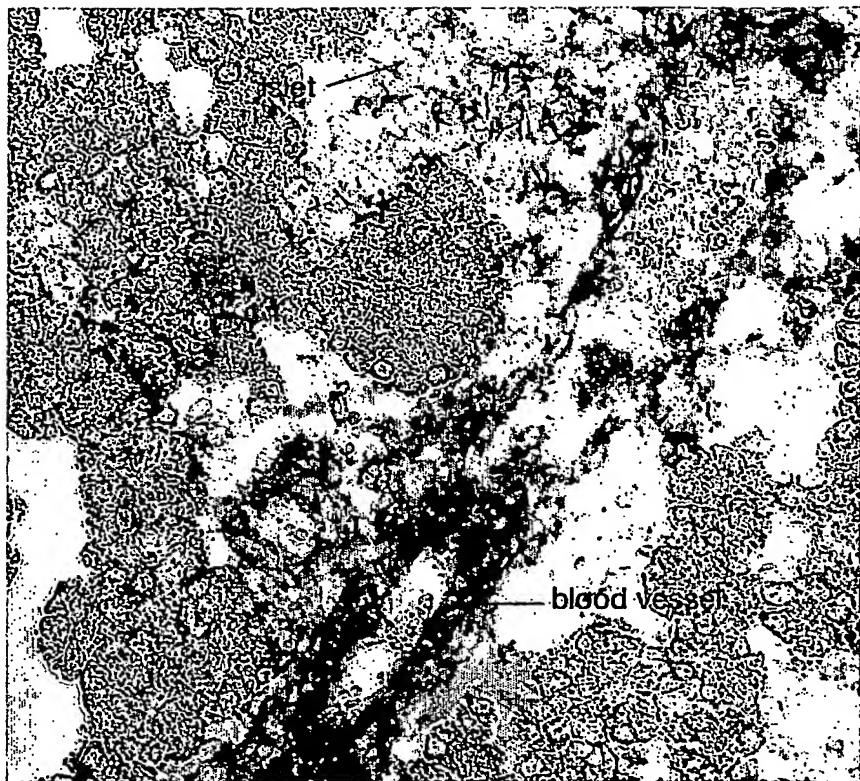


Fig. 4A

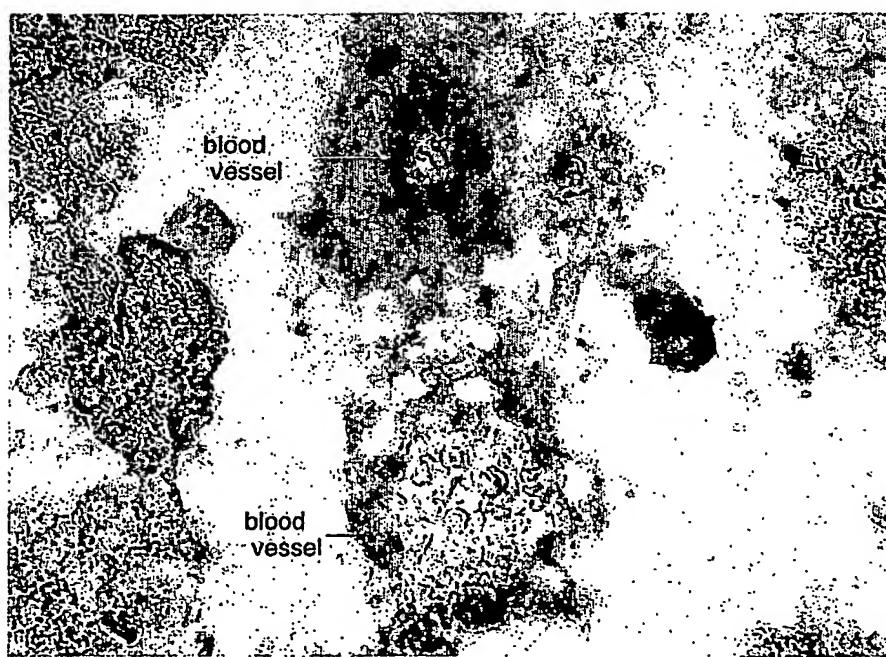
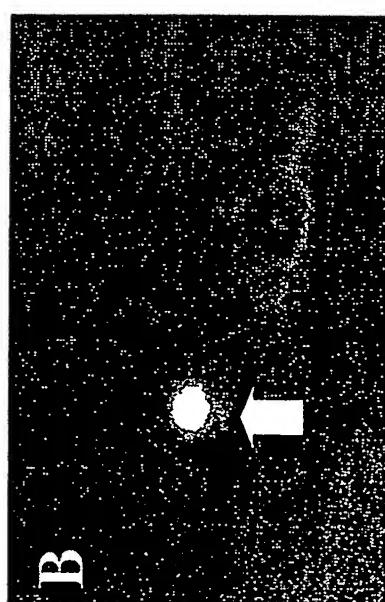
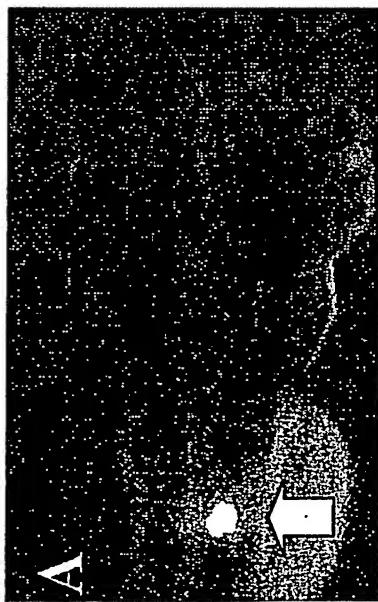
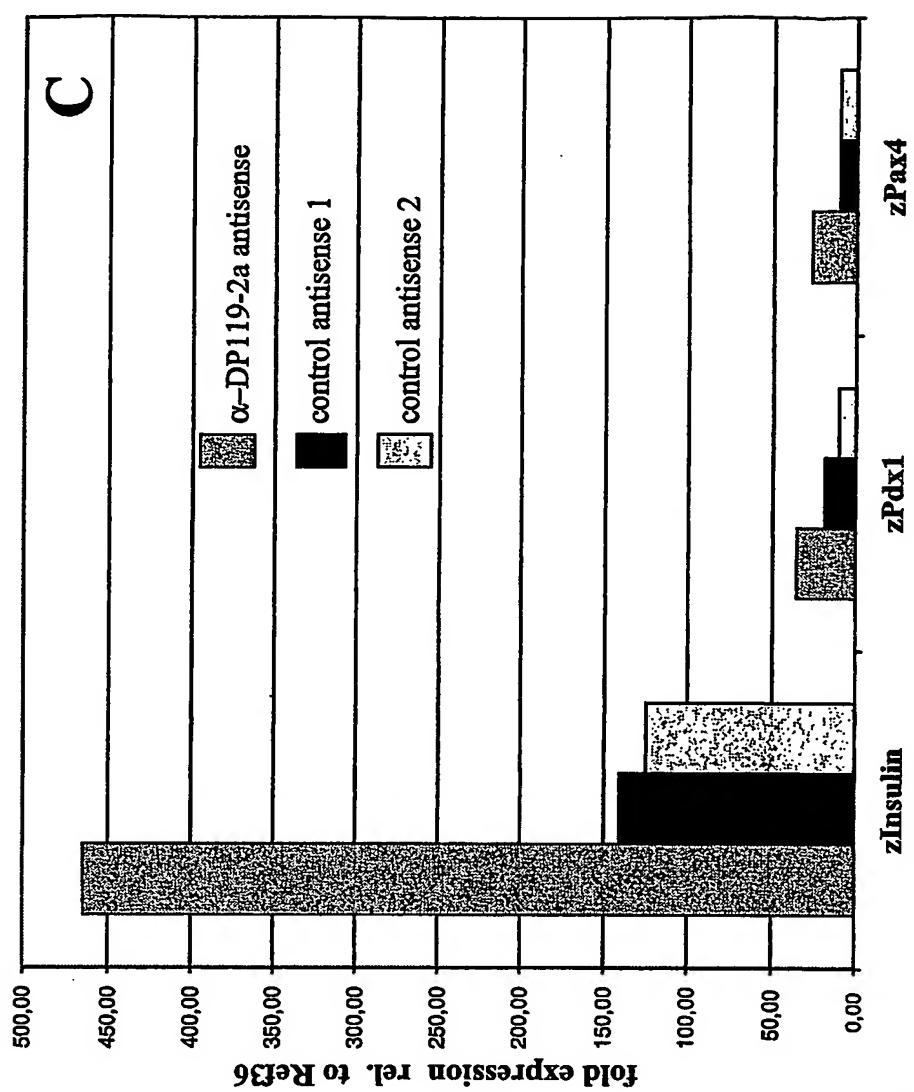


Fig. 4B

**Fig. 5**

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1 MTEMKIWCVL LMAFALTSAA PKSHLRLEEK TKDNNDTLQV EIDNOEHILS OLLGDYDKVK  
 61 ALSEGSDCGC KCVVRPLSAS ACQRIREGHA TPQDFYTVE ITSGPHCKCA CIAPPSALNP  
 121 CEGDFRLKKL RQAGKDNIKL STILELEGS FYGMDLLKIH SVTTKILDRE DTIEKMLN  
 181 QTEEKLNTIS TSPNPQLSTS SPPTLPSVIQ EKSTSLRQON DEAAAOFQHME SKYEKFVGD  
 241 ILNSGSDLNK ATTALQEQQ QGRKKQPKIT VRGITYYRSO PVDEMDSEKN LKETSAASSVT  
 301 QTGALIKEHL KASTQSTLNQ LTPSPSHSN ALTTESSVG INAHKGEVTT IVMTASVTGS  
 361 KTDSTVDTLTQ LSPRVRETLT TTRRTTKTAT TSQPVKRKYS ISWDEEEEAV VPEQVEEKA  
 421 VKPVVEDKVG EEPQRKPGTA HHQAKTISTV KQQIKFSLGM CKDTLATISE PITHINTYGRN  
 481 EGAWMKDPLD QDDKIYVTNY YYGNNLMLFR NIDVFKQGRF TNSYKLPYNW IGTGHVVYKG  
 541 AFYYNRAFSR DIIKFDLRLR YVAAWTMLHD AVFENDDVSS WRWRGNSDMD LAIDESGLWW  
 601 IYPALDDEGF LOEVIVLSSLR NPTDLMSKRE TTWRGTLRRN RYGNCFIVCG VLYATDSYNO  
 661 QDTNLSYAFD THNTQVIPH LPFSNNYTYV TQIDYNPKER VLYAWDNGHQ VTYNVQFAY

**Fig. 6A**

1 MGLLLHYIFCC VFCLTRANVE QQATDMDNR ATLEDEMDNQ ENILTQLIGD YDKVKTLSEG  
 61 SDCQCKCVVR PMSRSACKRI EEAQAKIEDF YTVEPVTAGP NCKKCACIAP PSALNPCEGD  
 121 FRFKKLQKTC QYDIKLSNM DLLEERVDNI EKEGEKGQKG ARSNORQEKK KRLSVVCWSL  
 181 HCRRTQQRLL LTLYRYRCXSV LEPSLQKNAA AAAFAHTEVQM QQFIPDQRKY EEKFVGNQGP  
 241 SKPVLLKSKS EGQEEQHKPA KTKADAKMS LRSMTFYKAN RMEDSEGEER DLIIEDQLH  
 301 QGLNTPVTTP EATVTVTQST TINLNTQNFT TARMSNVTKQ TQGQSVKAMM SSTI TTERPT  
 361 MPTSTTSTST MTPGTNTTTI ATPLUVPKQL ASVTVGQVSN SYKLPYNWIG TGHVVVYSGSF  
 421 FYNRAFSRDI IRFDLRLRYV AAWTTLHDAI LEEEAEAPWTW GGHSDIDFSV DESGLWLVYP  
 481 ALDDEGFHQE VIILSKLRAS DLQKEKSWRT GLRRNYYGNC FVICGVLYAV DSFERTHANI  
 541 SYAFDTHTHT OMIPRLPFIN NYTTTQIDY NPKERMLYAW DNGHQVTYDV IFAY

**Fig. 6B**

1 MWRIVELVAC LLMMSSHVS QSKIFGEEQV RMTSEGSDCR CKCIMRPLTR DACARLRTGS  
 61 VRVEDFYTVE TVSSGADCCKC SCTAPPSSLN PCENEWREK LKKQAPELLK LQSMVDLLEG  
 121 TLFSMDLLKV HSYINKVVSQ MNNLEE

**Fig. 6C**

1 MWIYASVLTY LLLLTRDARS LSKIFGEPEP VKMISEGSDC RCKCVMRPLS IEACSRRLDG  
 61 SLRVDDFYTV ETVSSGSDCK CSCTAPPSSL NPCENEWRTE KLXXQAPELL KLHSMVDLLE  
 121 GTLYSMDLMK VHAYMNKVVS QMNTLEEVMT IKTNLTRENE FVRDSVVNL NQLKRYENYS  
 181 DIMVSIKKEI SSLGLQOLLQK DAASDSKAQV GTESKKSKEA IKPPNKKPPA VKPPPQKPE  
 241 KPVPKKEAP AKAAPKAKPD PTTKTKTSVH QTGVIRGITY YKASKSE

**Fig. 6D**

DG119-1	Mm	-----MAYPLPLVLCFALVVAQVWGSTTPGTSEPPDVQTVPETEDDILQNEADNQEN	10	20	30	40	50	60
DG119-1	Hs	-----MAKPRLLVLYPALIVVPAWVSSIVLGTSEPPDAQTVAPAEDETLQNEADNQEN						
DG119-1a	Dr	-----MTEMKIWCVLLMMAFALTSAAPKS-----HLRLEEKTKDNNDTLOVEIDNQEH						
DG119-1b	Dr	-----MGLLLYIFCCVFCLTRAN-----VEQQATDNTDNRATLEDEMDNQEN						
DG119-2a	Dr	-----MWRIVELVACALLMMSS-----HVS						
DG119-2b	Dr	-----MWIYASVLTYLLLTR-----DAR						
DG119-2	Mm	MEAAAVLPRYLQLRLLLVLLLLVLRLRAG-----PVW						
DG119-2	Hs	MEAAAALPPRPLLPLVLLLSGR-----PTR						
----- Cystein rich domain -----								
DG119-1	Mm	VLSQLLGDYDKVKAVSEGSDCQCKCVVRPLGRDACQRINQGASRKEDFYTVETITSGSSC	70	80	90	100	110	120
DG119-1	Hs	VLSQLLGDYDKVKAMSEGSDCQCKCVVRPLGRDACQRINAGASRKEDFYTVETITSGSSC						
DG119-1a	Dr	ILSQLLGDYDKVKALSEGSDCGCKCVVRPLSASACQRIREGHATPQDFYTVETITSGPHC						
DG119-1b	Dr	ILTQLIGDYDKVKTLSEGSDCQCKCVVRPMRSACKRIEQAQAKIEDFYTVEPVTAGPNC						
DG119-2a	Dr	SQSKEFGE-EQVRMTEGSDCCRCKCIMRPLTRDACARLRTGSVRVEDFYTVETVSSGADC						
DG119-2b	Dr	SLSKIFGEPEPVKMISEGSDCCRCKCIMRPLSIEACSRSLRDGSLRVDDFYTVETVSSGADC						
DG119-2	Mm	PDSKVFSLDLQVVRTSEGSDCCRCKCIMRPLSKDACSRSVRSGRARVEDFYTVETVSSGADC						
DG119-2	Hs	ADSKVFGDLDQVVRTSEGSDCCRCKCIMRPLSKDACSRSVRSGRARVEDFYTVETVSSGADC						
----- Cystein rich domain -----								
DG119-1	Mm	K-CACVAPPSSAVNPCEGDFRLQKLREADSRDLK-----	130	140	150	160	170	180
DG119-1	Hs	K-CACVAPPSSALNPCEGDFRLQKLREADSQDLKVGPGMGQCLGRETFEIHKSGKAMVED						
DG119-1a	Dr	K-CACIAPPSSALNPCEGDFRLKLRQACKDNIK-----						
DG119-1b	Dr	KKCACIAPPSSALNPCEGDFRFKKLQKTTGQYDIK-----						
DG119-2a	Dr	K-CSCTAPPSSLNPCENEWKREKLKKQAPEELLKLQ-----						
DG119-2b	Dr	K-CSCTAPPSSLNPCENEWRTEKLKKQAPEELLKLH-----						
DG119-2	Mm	R-CSCTAPPSSLNPCENEWKMEKLKKQAPEELLKLQ-----						
DG119-2	Hs	R-CSCTAPPSSLNPCENEWKMEKLKKQAPEELLKKS-----						
----- Cystein rich domain -----								
DG119-1	Mm	-----LSTIID	190	200	210	220	230	240
DG119-1	Hs	SKPFEEGLSHFLTQTFRKAECTTYTIVLAYIPVYTNVFLTATSQFLASGFVPEPPLSTIID						
DG119-1a	Dr	-----LSTILE						
DG119-1b	Dr	-----LSNIMD						
DG119-2a	Dr	-----SMVD						
DG119-2b	Dr	-----SMVD						
DG119-2	Mm	-----SMVD						
DG119-2	Hs	-----						
-----								
DG119-1	Mm	MLEGAFYGLDLLKLHSVTTKLVG-----RVDKLEE	250	260	270	280	290	300
DG119-1	Hs	MLEGAFYGLDLLKLHSVTTKLVGRVDKLEEMLEGAFYGLDLLKLHSVTTKLVGRVDKLEE						
DG119-1a	Dr	LLEGSTFYGM DLLKLHSVTTKILD-----RMDTIK						
DG119-1b	Dr	LLEGSTFYGM DLLKLHSVTTKLL-----RVDNIK						
DG119-2a	Dr	LLEGTLFSMD DLLK VHSYINKVVS-----QMNNLEE						
DG119-2b	Dr	LLEGTLYSMD DLLK VHYAMNKVVS-----QMNTLEE						
DG119-2	Mm	LLEGALYSMD DLLK VHYIQKVAS-----QMNTLEE						
DG119-2	Hs	-----						
-----								
DG119-1	Mm	E--VSKNLTKENEQIKEDVEEIRTELN-KRGKENCSDNTLESMPDIRSALQRDAAA-----	310	320	330	340	350	360
DG119-1	Hs	E--VSKNLTKENEQIKEDMEEIRTEMN-KRGKENCSENILD SMPDIRSALQRDAAA-----						
DG119-1a	Dr	M--VLIQNQTEEKLNLTISTSPNP-----QLSTSS-----PTTLP SVI QEKST-----						
DG119-1b	Dr	S--FSGNLITKEKVSVKG EKG CQG-----KGARSNQRQEKKR LSVLEPSLQKNAAA-----						
DG119-2a	Dr	-----						
DG119-2b	Dr	VMTIKTNL TRENEFVRD SSVNLSNQLKRYEN YSDIM VS IKKE ISSLGLQ LLQKDAA-----						
DG119-2	Mm	S--IKANL SLENKVV KDSV HHLSEQLKSYEN QSAIMMSIKKELSSIGLQ LLQRDAAA VP A-----						
DG119-2	Hs	---IKANL SRENEVV KDSV RHLSEQLRHYEN HSIAIMLG IKKEL SRL GLQ LLQKDAAA APA-----						

Fig. 7

		370	380	390	400	410	420
DG119-1	Mm	-----AYAHP--EYEERFLQEETVSQQINSIELLRTQPLVPPAAMKPORFLQRQVHL					
DG119-1	Hs	-----AYAHP--EYEERFLQEETVSQQINSIELLQTPLALPEVVKSRPLQRQVHL					
DG119-1a	Dr	-----SLRQQN-DEAAAFQHMESEKYEEKFVGDIILNSGSDLNKATTALOE--OEOOGR					
DG119-1b	Dr	-----AFAHTE-VQMQQFI PDQRKYEEKFVGNQGPSKPVLKKSKSEGQE--EQHKPA					
DG119-2a	Dr						
DG119-2b	Dr	-----SDSKAQVGTESKKSKEAIKPPNKKPAVKKPPQPKPKVVKPKKEAPAKAAKPA					
DG119-2	Mm	TAPASSFDASKAQDTAGGQGRDLNKYGSIQKSFSDKGLAKPPKEKLLKVEKLR-KESIKGR					
DG119-2	Hs	TPATG-TGSKAQDTARGKGKDTSKYGSVQKSFADRGPLPKPKKEKLLQVEKLR-KESGKGS					
		430	440	450	460	470	480
DG119-1	Mm	-----RGRLASK-----PTVIRGITYYKAKVSEEENDIEQHDELFGSGDGVDLIEDQLLRQ					
DG119-1	Hs	-----RGRPASQ-----PTVIRGITYYKAKVSEEENDIEQHDEFFSGDNGVDLIEDQLLRH					
DG119-1a	Dr	-----KKQP-----KITVIRGITYYRSDPVDEMSEKNLKETSASSVTQTGALIKEHLKAS					
DG119-1b	Dr	-----KTKADAK-----NMRLRSMTFYKANRMEDSCEGEE-----RMDLIIEDQLHKQ					
DG119-2a	Dr						
DG119-2b	Dr	-----KPDPTTKTKTSVHQTGVIRGITYYKASKSE					
DG119-2	Mm	-----IPQPTARPRALAQQQAVIRGFTYYKAGRQEARQEAPKAAADSTLKGTWSLEKLPPK					
DG119-2	Hs	FLQPTAKPRALAQQQAVIRGFTYYKAGKQE-----VTEAVADNALQGTWSLEQLPPK					
		490	500	510	520	530	540
DG119-1	Mm	-----ED--LLTSATRRPATR-----HTAAVITDASIQAASSSEPAQASASASSFVEPAPQASDRE					
DG119-1	Hs	-----NG--LMTSVTRRPAATRQGHSTAVTSDLNARTAFWSSALPQPSTS DPSIANHASVGP-----					
DG119-1a	Dr	-----TQSTLNTLTPSPSTSNSALTVTESSVGINAHGEVTTIVMTASVTGSKTDVTDLTQLSP					
DG119-1b	Dr	-----G--LNTPVTTPEAT-----VTVTQSTT--INLNTQNFTTARMNSVTKQTQGQSVKAMMSS--					
DG119-2a	Dr						
DG119-2b	Dr						
DG119-2	Mm	-----IEAK--LPEPNSAKHDDVRLQASEGGNLTPIDTTTTSTSSSTTTTGTSTTSTTSTTS					
DG119-2	Hs	VEGRNSNSAEPNSAEQDEAEPRS SERVDLASFSTHLLILPPHSLHHHSTPVLATPAPFHLC					
		550	560	570	580	590	600
DG119-1	Mm	-----LLATPQTTVFPEPTG-----VMPSTQVSPPTVAHTAVQP-----LPAMVPGDIFVEALPLV					
DG119-1	Hs	-----TLQTTSVSPDPTRESVLOQSPQVPATTVAHTATQQPAAPAPPVSPREALMEAMHTV					
DG119-1a	Dr	-----RVRETLTTTRTTTKTA-----TTSQPVKRKYSISI SWDEEEE-----AVVP-EQVEEKAVK					
DG119-1b	Dr	-----TITTERPTMPTS-----TTSTSTMTPGTNTTTIATP-----LVVP-KQLAR--					
DG119-2a	Dr						
DG119-2b	Dr						
DG119-2	Mm	-----TTTPSP-----					
DG119-2	Hs	HNKPVPSPRRWQTPSRALPGWSNCRPRWRAGPTPQSPTQSRMRLSPGPPSEWTWLLAP					
		610	620	630	640	650	660
DG119-1	Mm	-----PLLPTVGTDMPEEGTAGQEATSAGPILSPEEEDDIRNVIG-----					
DG119-1	Hs	-----PVPPPTVRTDSLGDAPAGWGTTPASPTLSPEEEDDIRNVIG-----					
DG119-1a	Dr	-----PVVEDKVGEEPQRKPGTAHHQAKTISTVKQOIKFSLG-----					
DG119-1b	Dr						
DG119-2a	Dr						
DG119-2b	Dr						
DG119-2	Mm	-----ITTPWPTEPPLHPEVPSQGRED-----					
DG119-2	Hs	HFNPCHHHHRHPHPQPPPTSSLTEPPSGPEVSSQGRE-----					
		670	680	690	700	710	720
		730	740	750	760	770	780
DG119-1	Mm	-----RCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDDRIYVTNYYYGNTLVEFRNLEN					
DG119-1	Hs	-----RCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYYGNTLVEFRNLEN					
DG119-1a	Dr	-----MCKDTLATICEPITHNTYGRNEGAWMKDPLDQDDKIYVTNYYYGNNLLEFRNIDV					
DG119-1b	Dr	-----ICKDTLASISDPVTHNKYGRNEGAWMKDPKGNGKVYYTDYYYYGNQLLEFRDIDT					
DG119-2a	Dr						
DG119-2b	Dr						
DG119-2	Mm	-----SCEGTLRAVDPPVKHHHSYGRHEGAWMKDPAAALDDRIVTNYYYGNSLVEFRNLEN					
DG119-2	Hs	-----SCEGTLRAVDPPVRHHHSYGRHEGAWMKDPAAARDDRIVTNYYYGNSLVEFRNLEN					

| ----- Olfactomedin-like domain -----

Fig. 7 (cont.)

		790	800	810	820	830	840	
DG119-1	Mm	FKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNRAFTRNIKYDLKQRYVAAWAMLHDVAYE						
DG119-1	Hs	FKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNRAFTRNIKYDLKQRYVAAWAMLHDVAYE						
DG119-1a	Dr	FKQGRFTNSYKLPYNWIGTGHVVYKGAFYNNRAFSRDIKYDLRLRYVAAWTMLHDAILE						
DG119-1b	Dr	FKQGQVSNSYKLPYNWIGTGHVVYSGSFFYNRAFSRDIKYDLRLRYVAAWTMLHDAILE						
DG119-2a	Dr							
DG119-2b	Dr							
DG119-2	Mm	FKQGRWSNSMYKLPYNWIGTGHVVYQGAFYYNRAFTKNIKYDLRQRFVASWALLPDVVYE						
DG119-2	Hs	FKQGRWSNSMYKLPYNWIGTGHVVYQGAFYYNRAFTKNIKYDLRQRFVASWALLPDVVYE						
		Olfactomedin-like domain						
		850	860	870	880	890	900	
DG119-1	Mm	--EATPWRWQGHSDVDFAVDENGLWLIPALDD-EGFNQEIVI VLSKLNADLSTOKETTW						
DG119-1	Hs	--EATPWRWQGHSDVDFAVDENGLWLIPALDD-EGFSQEIVI VLSKLNADLSTOKETTW						
DG119-1a	Dr	NDVSSWRWRGNSDMDLAIDESGLWVIYPALDD-EGFLQEVIVLSRINPTDLSMKRETTW						
DG119-1b	Dr	-EEEAPWTWGGHSIDF SVDESGLWLVPALDD-EGFHQEVIILSKLRASDL--QKEKSW						
DG119-2a	Dr							
DG119-2b	Dr							
DG119-2	Mm	--DTTPWKWRGHSDIDFAVDESGLWVIYPAVDEHDETQHEVIVLSRLDPADLSVHRETTW						
DG119-2	Hs	--DTTPWKWRGHSDIDFAVDESGLWVIYPAVDDRDEAQPEVIVLSRLDPGDL SVHRETTW						
		Olfactomedin-like domain						
		910	920	930	940	950	960	
DG119-1	Mm	RTGLRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPRLLFENEYSYTTQI						
DG119-1	Hs	RTGLRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPRLLFENEYSYTTQI						
DG119-1a	Dr	RTGLRRNRGYGNCFVICGVLYATDSYNQDNTLNSYAFDTHTNTQVIPHLPFSNNYTYVTQI						
DG119-1b	Dr	RTGLRRRNYYGNCFVICGVLYAVDSFERTHANISYAFDTHTQMI PRLPFINNNYTYTTQI						
DG119-2a	Dr							
DG119-2b	Dr							
DG119-2	Mm	KTRLRRNSYGNCFLVCGILYTVDTYNQHEGQVAYAFDTHTGTDAPHQLPFLNEYSYTTQV						
DG119-2	Hs	KTRLRRNSYGNCFLVCGILYTVDTYNQQEGQVAYAFDTHTGTDARPQLPFLNEHAYTTQI						
		Olfactomedin-like domain						
		970	980	990	1000	1010	1020	
DG119-1	Mm	DYNPKDRLLYAWDNGHQVITYHVIFAY						
DG119-1	Hs	DYNPKDRLLYAWDNGHQVITYHVIFAY						
DG119-1a	Dr	DYNPKERVLYAWDNGHQVITYNVQFAY						
DG119-1b	Dr	DYNPKERMLYAWDNGHQVITYDVIF--						
DG119-2a	Dr							
DG119-2b	Dr							
DG119-2	Mm	DYNPKERVLYAWDNGHQLTYTLHFVV						
DG119-2	Hs	DYNPKERVLYAWDNGHQLTYTLHFVV						
		Olfactomedin-like dom.--						

Fig. 7 (cont.)

**rIP-mDG119-1 tg mice**

0.8kb rat insulin II promoter

*mDG119-1*

2.2 kb

hybrid  
intron

bgh-polyA

**Fig. 8A****Pdx1-mDG119-1 tg mice**

4.3kb mouse Pdx1-promoter

*mDG119-1*

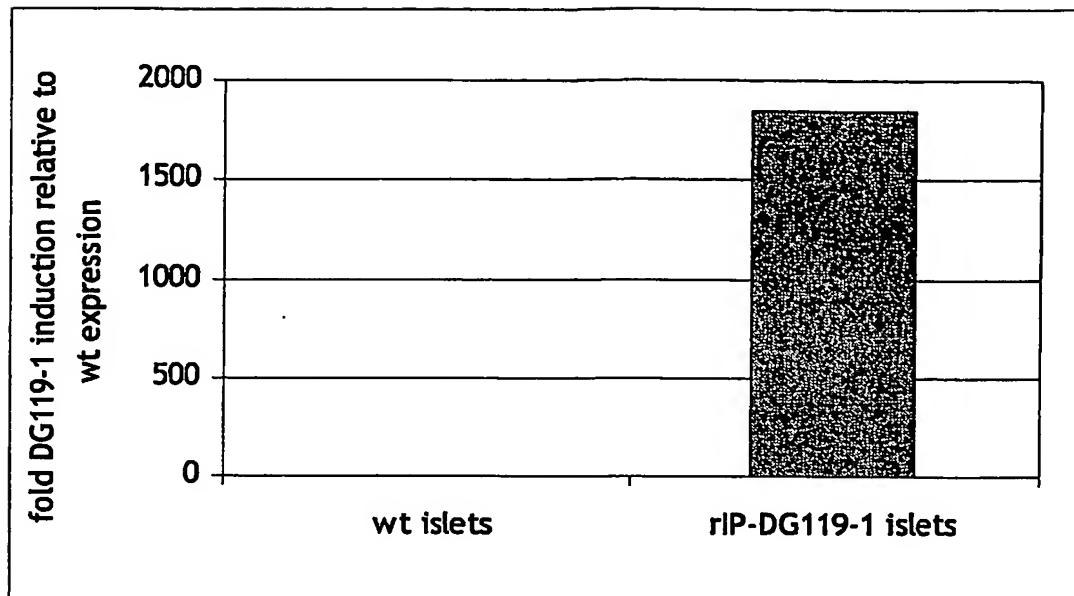
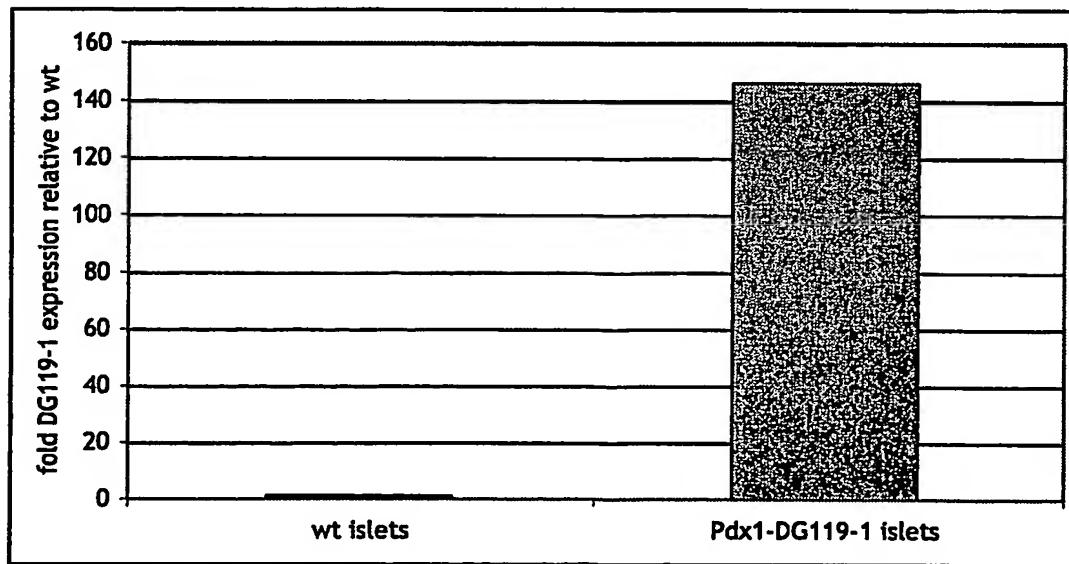
2.2kb

hybrid  
intron

bgh-polyA

**Fig. 8B**

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**Fig. 9A****Fig. 9B**

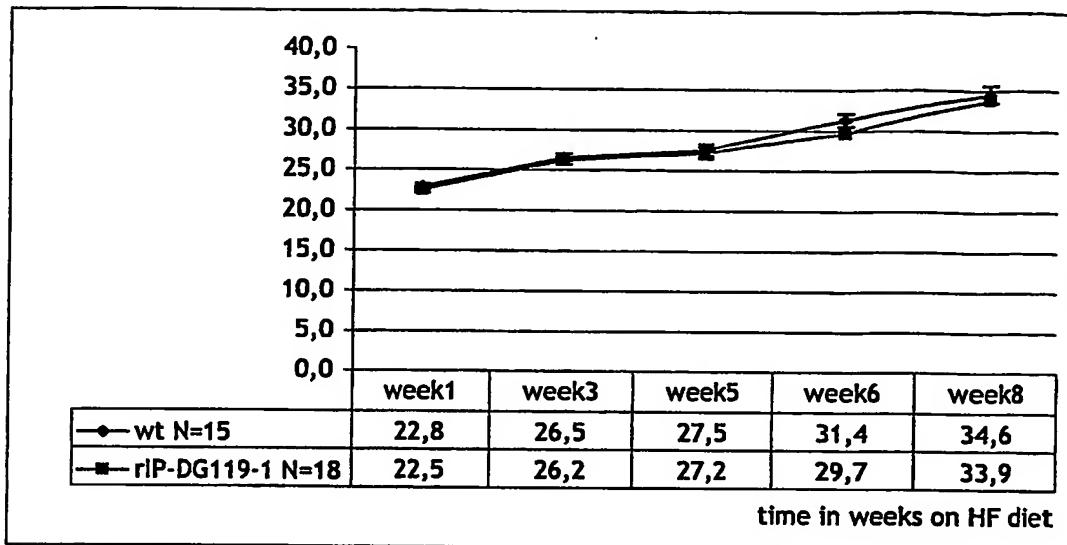


Fig. 10A

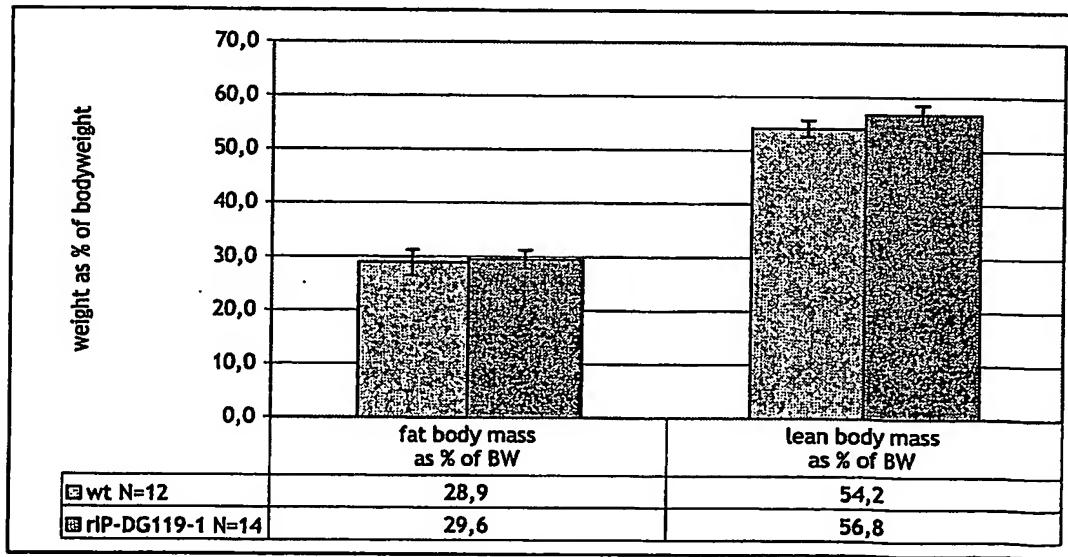


Fig. 10B

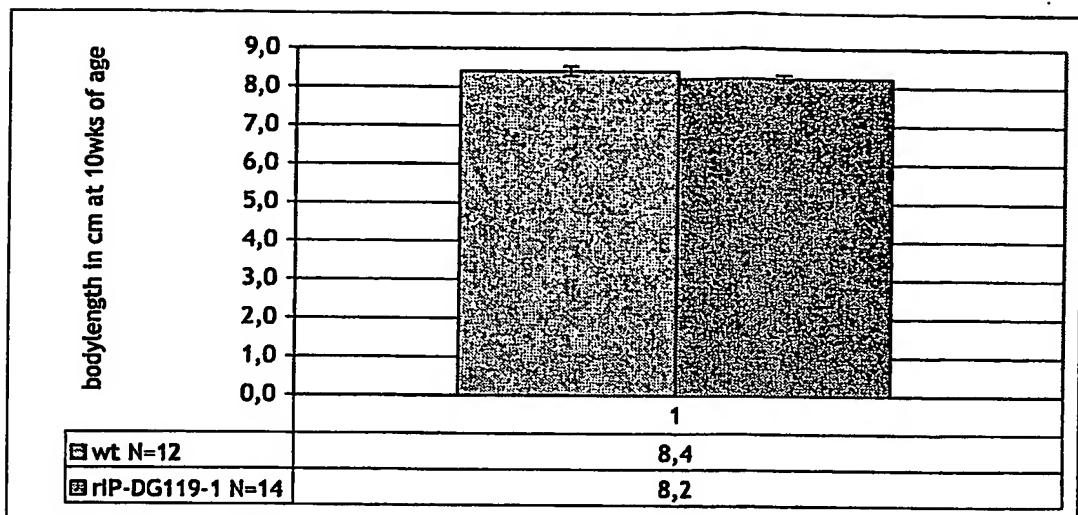


Fig. 11

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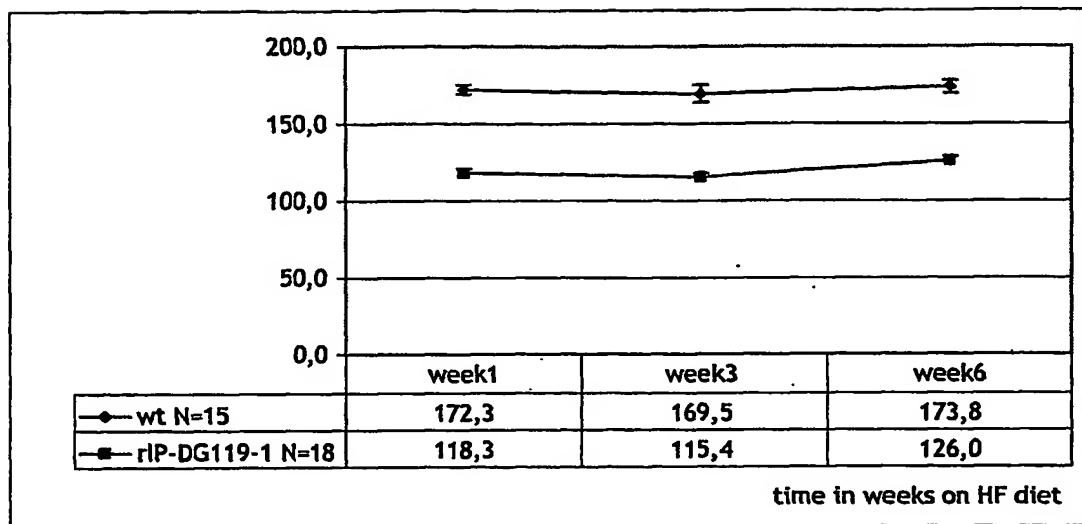


Fig. 12A

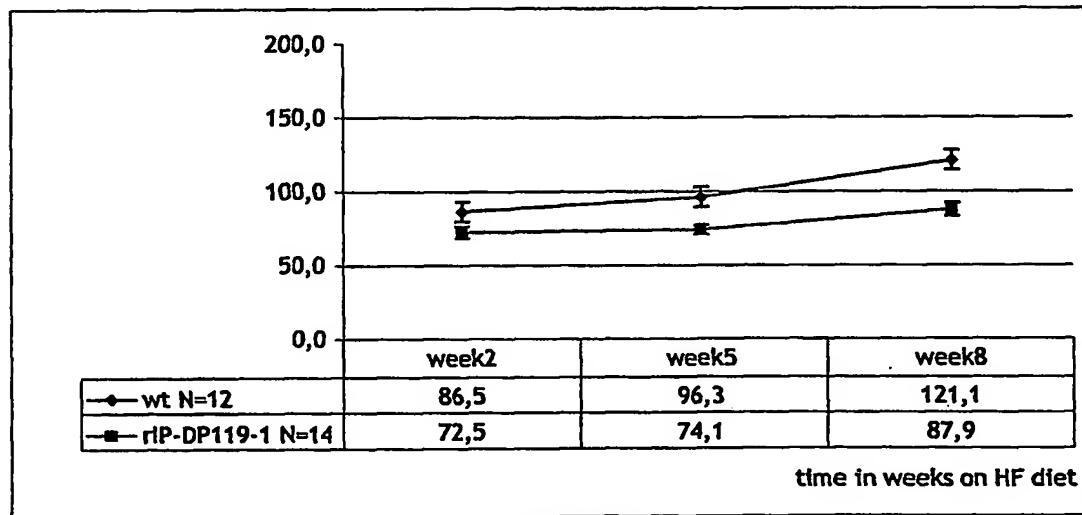


Fig. 12B

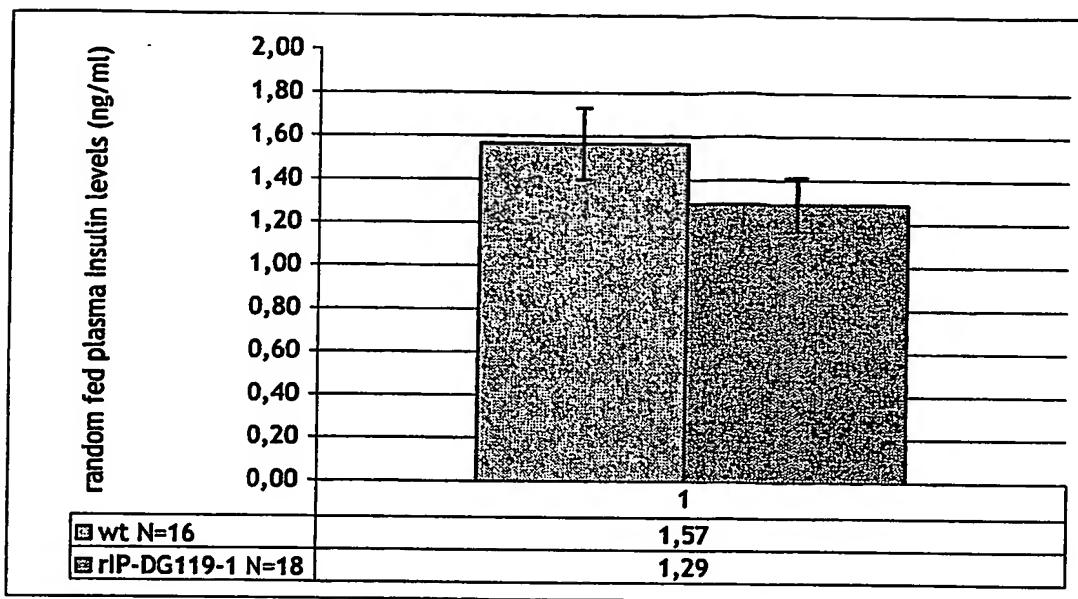


Fig. 13A

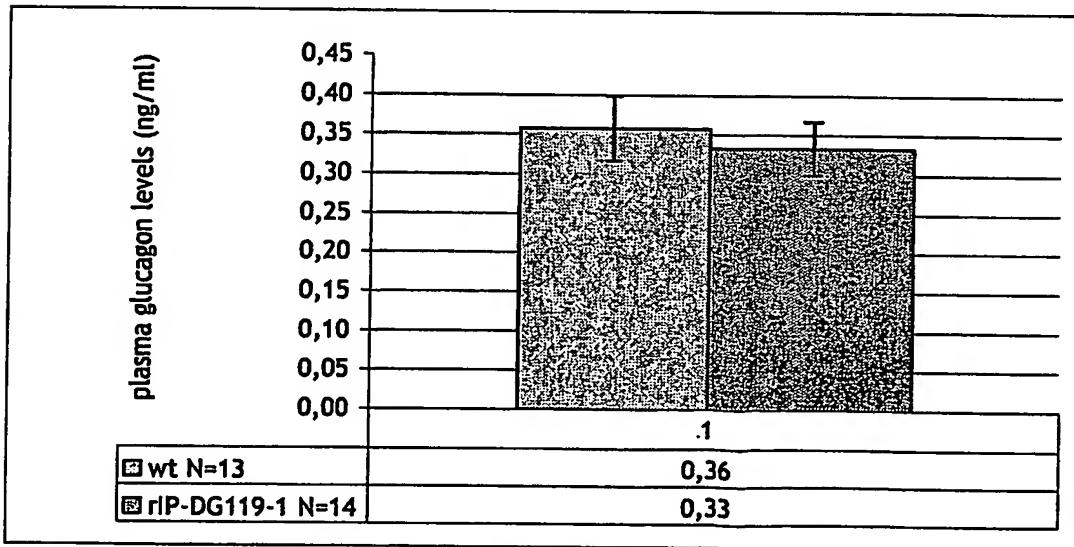


Fig. 13B

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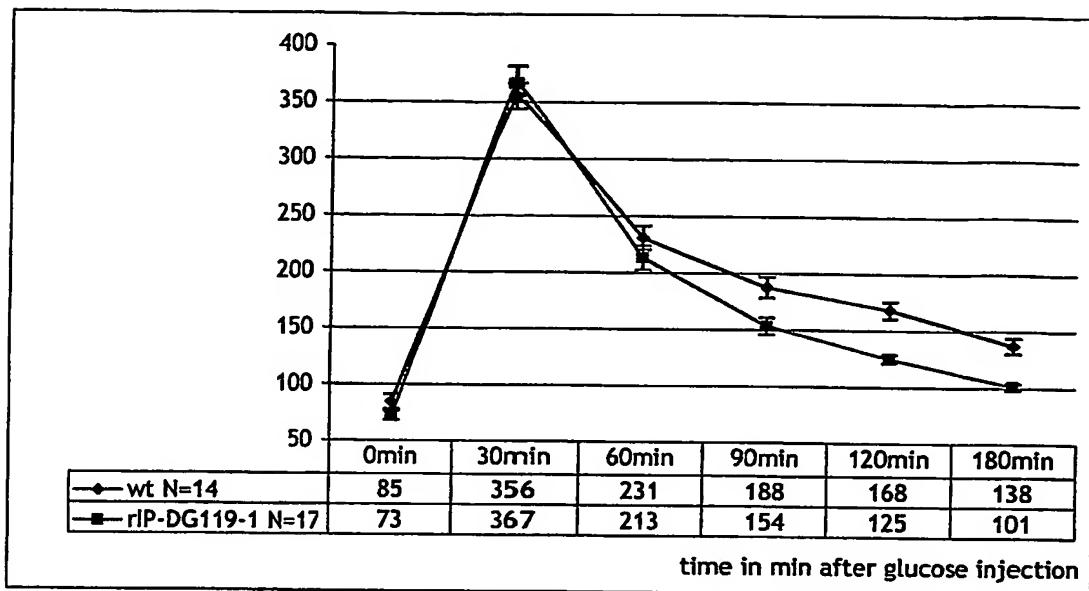


Fig. 14A

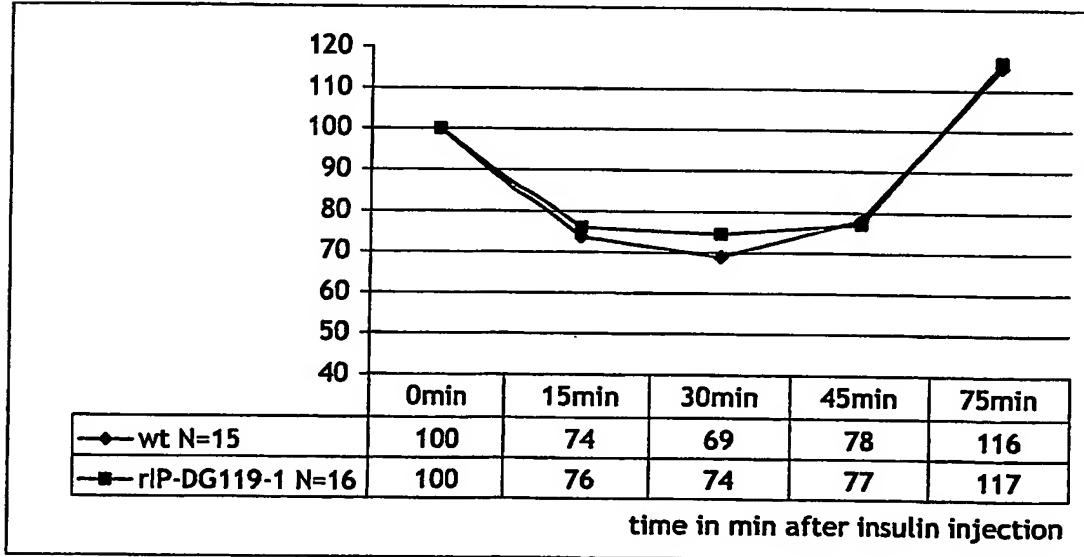


Fig. 14B

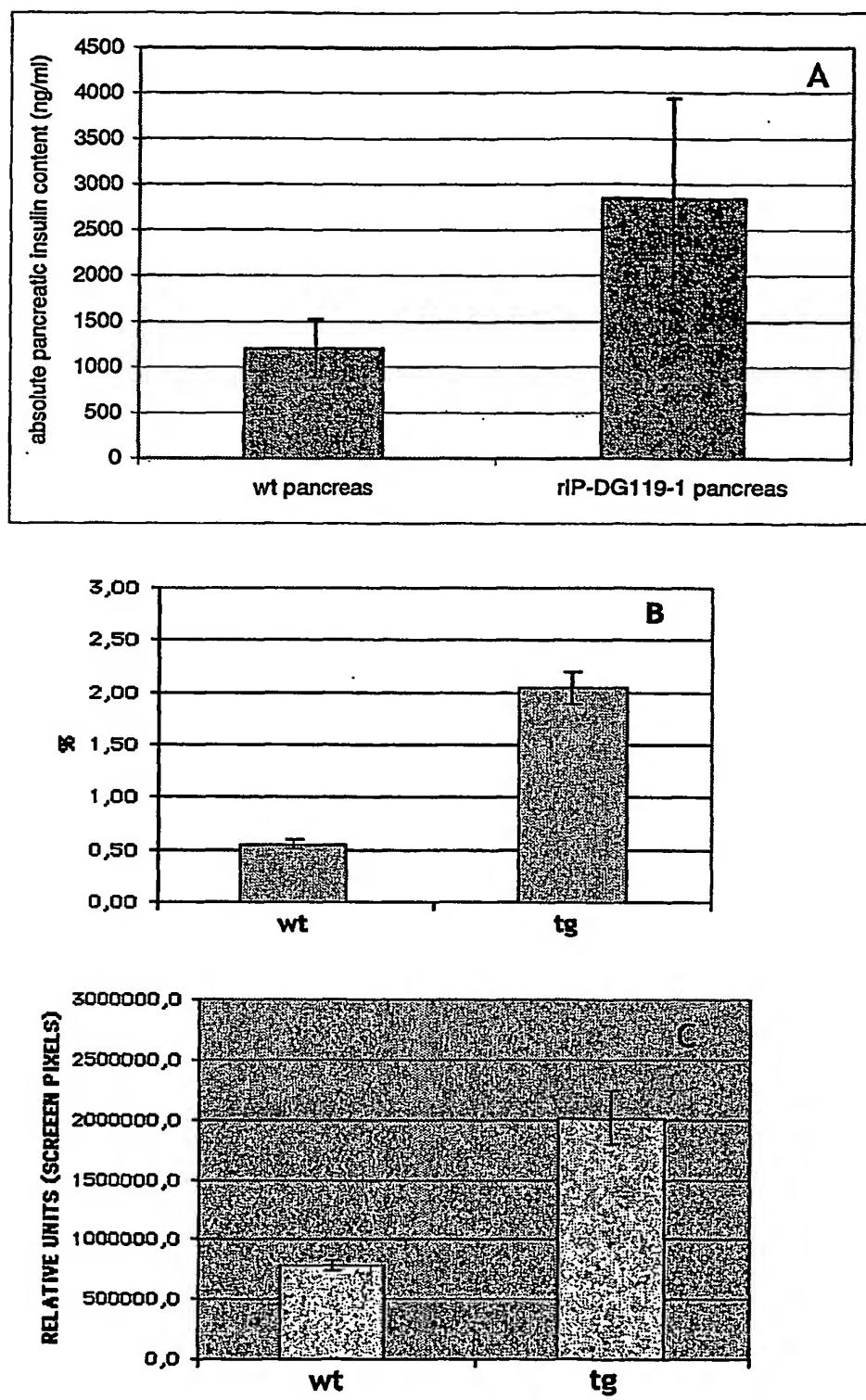


Fig. 15

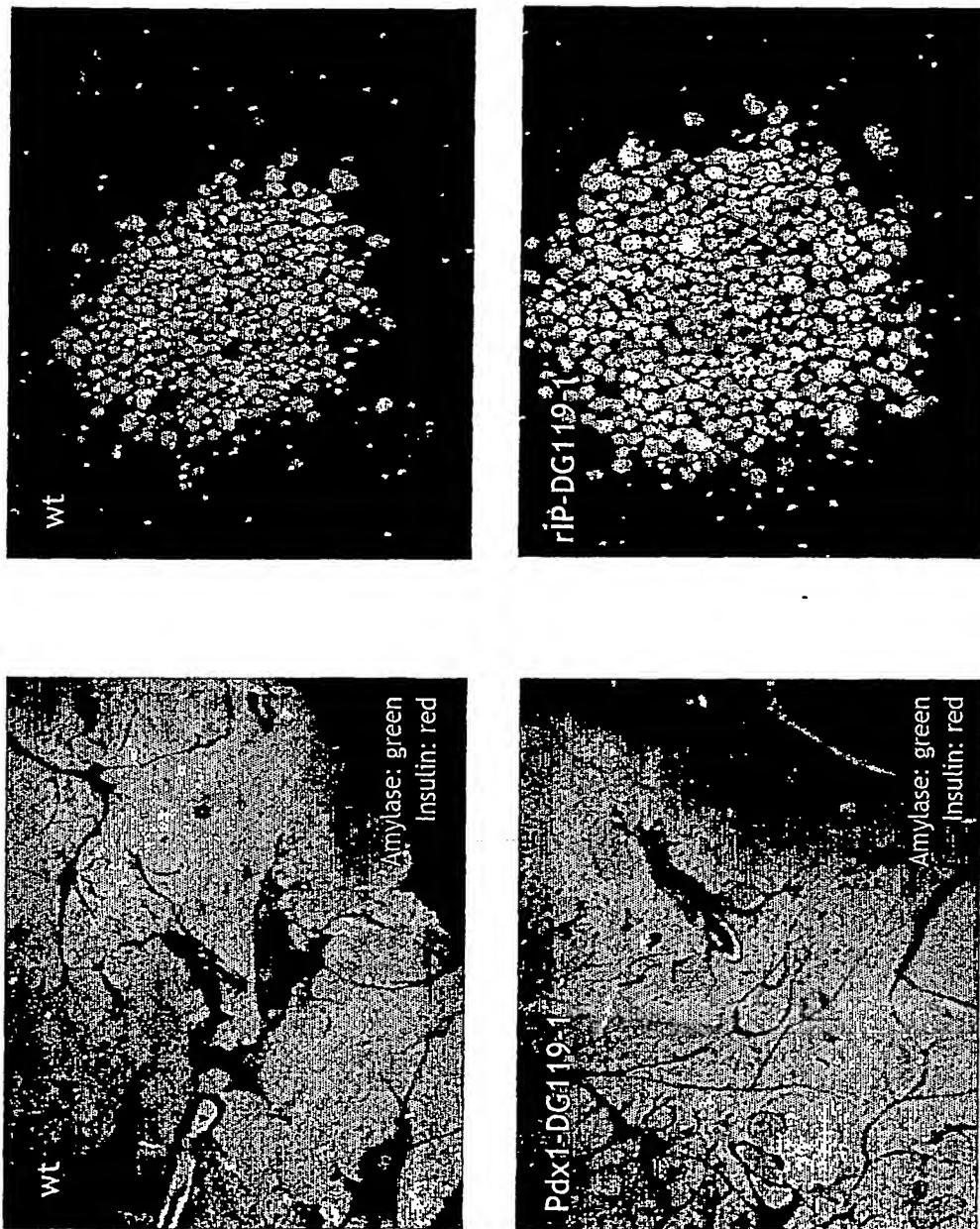


Fig. 16

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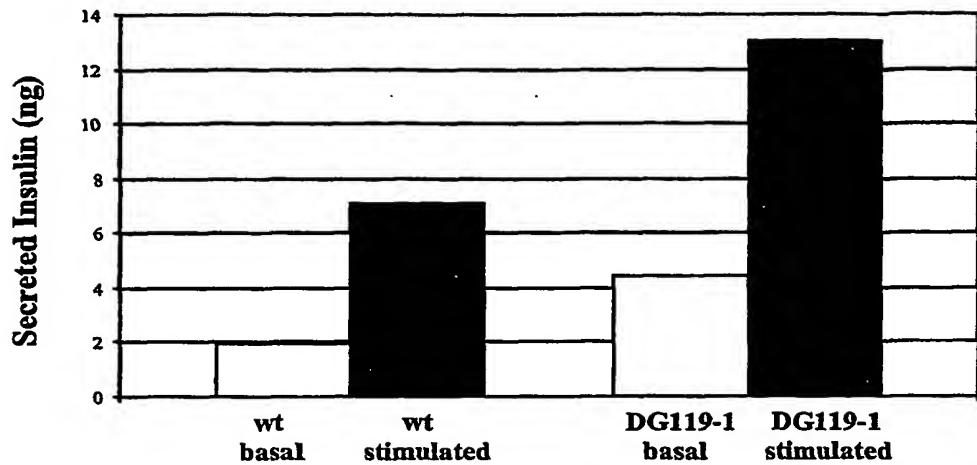


Fig. 17